FIGURE 1

Fucosyltransferase nucleotide sequence from strain 1182 FutB (SEQ ID NO:1)

atgttccaacccctattagacgcttatatagaaagcgcttccattgaaaaaattacctctaaatctcccccccccctaaaaatcgctg
tggcgaattggtggggagatgaagaggttgaagaatttaaaaagaacattctttattttattctcagtcagcattacacaatcaccct
ccaccaaaaccccaacgaaccctccgatctcgtctttggcagtcctattggatcagccagaaaaatcttatcctatcaaaacgcaa
aaagagtgttttacaccggtgaaaacgaatcgcctaatttcaacctctttgattacgccataggctttgatgaattggattttagagat
cgttatttaagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccacttcgccttacaaactcaaac
ctgacagcctttatgctttaaaaaaaacccctcccatcattttaaagaaaaccaccccaatttatgcgcagtagtgaacaatgagagcg
atcctttgaaaagaggggtttgcgagttttgtagcgagcaaccctaacgctcctaaaaggaatgctttctatgacgtttaaattctata
gagccagttattgggggagggagcgtgaaaaacactttaggctataacattaaaaacaagagcgagttttaagccaatacaaat
tcaatctgtgtttgaaaactcacaaggctatggctatgtaactgaaaaaatcattgacgcttactttagccataccattcctatttattg
ggggagtcctagcgtggcacaagattttaaccctaagagtttgtgaatgtttgtgattttaaagattttgatgaagcgattgatcatgt
gcgatacttgcacacgcacccaaacgcttatttagacatgctttatgaaaacccttaaacacccttgatgggaaagcttacttttac
caaaatttgagttttaaaaaaatcctagatttttttaaaacgattttagaaaacgacacgatttatcacgataacccttttattttttatcgt
gatttgaatgagccgttaatatctattgatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaatta
tgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgattt
gagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgagcggctcttaca
aaacgcctcgcctttattagaactctctcaaaacaccactttaaaatctatcgcaaagcttatcaaaaatccttacctttgttgcgtgc
ggcgagaaagttgattaaaaaattgggtttgtaa

Protein sequence from strain 1182 FutB (SEQ ID NO:2)

mfqplldayiesasiekitskspppikiavanwwgdeeveefkknilyfilsqhytitlhqnpnepsdlvfgspigsarkilsy
qnakrvfytgenespnfnlfdyaigfdeldfrdrylrmplyydrlhhkaesvndttspyklkpdslyalkkpshhfkenhpnl
cavvnnesdplkrgfasfvasnpnapkrnafydvlnsiepvigggsvkntlgyniknkseflsqykfnlcfensqgygyvte
kiidayfshtipiywgspsvaqdfnpksfvnvcdfkdfdeaidhvrylhthpnayldmlyenplntldgkayfyqnlsfkki
ldffktilendtiyhdnpfifyrdlneplisidddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlrvnydd
lrvnyddlrvnyddlrvnyddlrvnyerllqnaspllelsqnttfkiyrkayqkslpllraarklikklgl*

FIGURE 2

Fucosyltransferase from strain 1111 FutA

Nucleotide coding sequence (SEQ ID NO:3)

atgttccaaccccctattagatgcctttatagaaagcgctccattgaaaaaatggcctctaaatctccccccccctaaaaatcgctgtgg
cgaattggtgggggagatgaagaaattaaaaaatttaaaaagagcgttctttattttatcctaagccagcattacacaatcactttaca
ccgaaaccctgataaacctgcggacatcgtctttggtaaccccccttggatcagccagaaaaatcttatcctatcaaaacgcaaaaa
gggtgttttacaccggtgaaaatgaagtccctaacttcaacctctttgattacgccataggctttgatgaattggactttagagatcgt
tatttgagaatgcctttgtattatgcctatttgcattataaagccgagcttgttaatgacaccacttcgccttataaactccaacctgaca
gcctttatgctttaaaaaaaccctcccatcatttaaagaaaaccaccccaatttgtgcgcagtagtgaataatgagagtgatcctttg
aaaagagggtttgcgagctttgtcgcaagcaaccctaacgctcctagaaggaacgcttttatgaggctttaaacgctattgagcc
agttgctgggggagggagcgtgaaaaacactttaggctataatgtcaaaaacaagagcgagtttttaagccaatacaaattcaat
ctgtgttttgaaaacactcaaggctatggctatgtaactgaaaagatcattgacgcttatttcagccataccattcctatttattggggg
agtcccagcgtggcgaaagattttaaccctaagagttttgtgaatgtccatgatttcaacaactttgatgaagcgattgactatatca
gatacttgcacacgcacccaaacgcttatttagacatgcactatgaaaacccctttaaacactattgatgggaaagcttacttttacca
aaatttgagttttaaaaaaatcctagattttttttaaaacgatttttagaaaacgacacgatctatcacgataacccctttcattttctatcgtg
atttgaatgagccttcagtatctattgatggtttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgat
gatttgagggttaattatgagcgcctttacaaaacgcctcgcctttattagaactctctcaaaacaccactttaaaatctatcgcaaa
gcttatcaaaaatccttgcctttgttgcgtgccataaggagatgggttaaaaagtaa

Protein sequence (SEQ ID NO:4)

mfqplldafiesaplkkwplnlpplkiavanwwgdeeikkfkksvlyfilsqhytitlhrnpdkpadivfgnplgsarkilsy
qnakrvfytgenevpnfnlfdyaigfdeldfrdrylrmplyyaylhykaelvndttspyklqpdslyalkkpshhfkenhpn
lcavvnnesdplkrgfasfvasnpnaprrnafyealnaiepvagggsvkntlgynvknkseflsqykfnlcfentqgygyvt
ekiidayfshtipiywgspsvakdfnpksfvnvhdfnnfdeaidyirylhthpnayldmhyenplntidgkayfyqnlsfk
kildffktilendtiyhdnpfifyrdlnepsvsidglrvnyddlrvnyddlrvnyddlrvnyerllqnaspllelsqnttfkiyrka
yqkslpllrairrwvkk*

FIGURE 3

Strain 1218 FutB nucleotide sequence (SEQ ID NO:5)

atgttccaacccctattagacgcttatatagaaagcgcttccattgaaaaaattacctctaaatctcccccccccctaaaaatcgctg
tggcgaattggtggggagatgaagaggttgaagaatttaaaaagaacattctttattttattctcagtcagcattacacaatcaccct
ccaccaaaaccccaacgaaccctccgatctcgtctttggcagtcctattggatcagccagaaaaatcttatcctatcaaaacgcaa
aaagagtgtttacaccggtgaaaacgaatcgcctaatttcaacctctttgattacgccataggctttgatgaattggatttttagagat
cgttatttaagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccacttcgccttacaaactcaaac
ctgacagcctttatgctttaaaaaaaccctcccatcattttaaagaaaaccaccccaatttatgcgcagtagtgaacaatgagagcg
atcctttgaaaagagggtttgcgagttttgtagcgagcaaccctaacgctcctaaaaggaatgctttctatgacgctttaaattctata
gagccagttattggggagggagcgtgaaaaacactttaggctataacattaaaaacaagagcgagttttaagccaatacaaat
tcaatctgtgttttgaaaactcacaaggctatggctatgtaactgaaaaaatcattgacgcttactttagccataccattcctatttattg
ggggagtcctagcgtggcacaagattttaaccctaagagttttgtgaatgtttgtgattttaaagattttgatgaagcgattgatcatgt
gcgatacttgcacacgcacccaaacgcttatttagacatgctttatgaaaacccttaaacacccttgatgggaaagcttacttttac
caaaatttgagttttaaaaaaatcctagatttttttaaaacgatcttagaaaacgacacgatttatcacgataaccctttatttttatcgt
gatttgaatgagccgttaatatctattgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatga
tgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttgagggttaattatgatgatttga
gggttaattatgatgatttgagggttaattgtgatgatttgagggttaattatgatgatttgagggttaattatgagcggctcttacaaa
acgcctcgcctttattagaactctctcaaaacaccacttttaaaatctatcgcaaagcttatcaaaaatccttacctttgttgcgtgcgg
cgagaaagttgattaaaaaattgggtttgtaa

Predicted protein strain 1218 FutB (SEQ ID NO:6)

mfqplldayiesasiekitsksppplkiavanwwgdeeveefkknilyfilsqhytitlhqnpnepsdlvfgspigsarkilsy
qnakrvfytgenespnfnlfdyaigfdeldfrdrylrmplyydrlhhkaesvndttspyklkpdslyalkkpshhfkenhpnl
cavvnnesdplkrgfasfvasnpnapkrnafydalnsiepvigggsvkntlgyniknkseflsqykfnlcfensqgygyvte
kiidayfshtipiywgspsvaqdfnpksfvnvcdfkdfdeaidhvrylhthpnayldmlyenplntldgkayfyqnlsfkki
ldffktilendtiyhdnpfifyrdlneplisiddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlrvnyddlr
vnyddlrvncddlrvnyddlrvnyerllqnaspllelsqnttfkiyrkayqkslpllraarklikklgl*

FIGURE 4

<u>Fucosyltransferase strain 19C2 FutB nucleotide sequence (SEQ ID NO:7)</u>

atgttccaaccccctattagacgcttatatagacagcacccgtttagatgaaaccgattataagcccccattaaatatagccctagcg
aattggtggcctttggataaaagagagaaagcaaagggtttagaaaaaaaatttatcttacatttcattttaagtcagcattacacaatcgc
tctccaccgaaaccctgataaaacctgcggacatcgtttttggtaacccccttggatcagccagaaaaatcctatcctatcaaaacg
ctaaaagggtgtttacaccggtgaaaacgaagtccctaatttcaacctctttgattacgccataggctttgatgaattggactttaga
gatcgttatttgagaatgcctttatattatgatagactacaccataaagccgagagcgtgaatgacaccaccgcaccttacaagatt
aaatctgacagcctttatgctttaaaaaagccctcccatcattttaaagaaaaccacccacatttatgcgcgctaatcaataatgaga
tcgatcctttgaaaagagggtttgcgagctttgtcgcaagcaaccctaacgcccctataaggaacgctttctatgaggctttaaattc
tattgagccagttactgggggagggagcgtgagaaacactttaggctataacgtcaaaaacaaaaacgaatttttgagccaatac
aagttcaatctgtgctttgaaaacactcaaggctatggctatgttactgaaaaaatcattgacgcttacttcagccacaccattcctat
ttattggggggggagtccctagcgtggcgaaagattttaaccccc

<u>Strain 19C2 FutB protein sequence (SEQ ID NO:8)</u>

mfqplldayidstrldetdykpplnialanwwpldkreskgfrkkfilhfilsqhytialhrnpdkpadivfgnplgsarkilsy
qnakrvfytgenevpnfnlfdyaigfdeldfrdrylrmplyydrlhhkaesvndttapykiksdslyalkkpshhfkenhph
lcalinneidplkrgfasfvasnpnapimafyealnsiepvtgggsvmtlgynvknkneflsqykfnlcfentqgygyvtek
iidayfshtipiywggvpsvakdfnp

FIGURE 5

Strain 915 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:9)

atggcctctaaatctccccccctaaaaatcgctgtggcgaattggtggggagatgaagaaattaaaaaatttaaaaagagcgttct
ttattttatcctaagccagcattacacaatcactttacaccgaaaccctgataaacctgcggacatcgtctttggtaaccccccttggat
cagccagaaaaatcttatcctatcaaaacgcaaaaagggtgttttacaccggtgaaaatgaagtccctaacttcaacctctttgatta
cgccataggcttt

Protein sequence from Strain 915 FutA (SEQ ID NO:10)

maskspplkiavanwwgdeeikkfkksvlyfilsqhytitlhrmpdkpadivfgnplgsarkilsyqnakrvfytgenevpn
fnlfdyaigf

FIGURE 6

Strain 26695 FutA fucosyltransferase nucleotide coding sequence (SEQ ID NO:11)

atgttccaaccccctattagacgcctttatagaaagcgcttccattgaaaaaatggcctctaaatctcccccccccccccctaaaaatc
gctgtggcgaattggtgggggagatgaagaaattaaagaatttaaaaagagcgttctttattttatcctaagccaacgctacgcaatc
accctccaccaaaacccccaatgaattttcagatctagtttttagcaatcctcttggagcggctagaaagattttatcttatcaaaacac
taaacgagtgttttacaccggtgaaaacgaatcacctaatttcaacctctttgattacgccataggctttgatgaattggattttaatga
tcgttatttgagaatgccttgtattatgcccatttgcactataaagccgagcttgttaatgacaccactgcgccctacaaactcaaag
acaacagcctttatgctttaaaaaaaaccctctcatcatttaaagaaaaccaccctaatttgtgcgcagtagtgaatgatgagagcg
atcttttaaaaagagggtttgccagttttgtagcgagcaacgctaacgctcctatgaggaacgcttttttatgacgctctaaattccata
gagccagttactgggggaggaagtgtgagaaacactttaggctataaggttggaaacaaaagcgagttttttaagccaatacaagt
tcaatctctgttttgaaaactcgcaaggttatggctatgtaaccgaaaaaaatccttgatgcgtattttagccataccattcctatttattg
ggggagtcccagccgtggcgaaagattttaaccctaaaagttttgtgaatgtgcatgatttcaacaactttgatgaagcgattgattat
atcaaatacctgcacacgcacccaaacgcttatttagacatgctctatgaaaacccctttaaacacccttgatgggaaagcttactttt
accaagatttgagtttttaaaaaaaatcctagatttttttttaaaacgatttttagaaaacgatacgatttatcacaaattctcaacatctttcatg
tgggagtacgatctgcataagccgttagtatccattgatgatttgagggttaattatgatgatttgagggttaattatgaccggctttta
caaaacgcttcgcctttattagaactctctcaaaacaccacttttaaaatctatcgcaaagcttatcaaaaatccttgcctttgttgcgc
gcggtgagaaagttggttaaaaaaattgggtttgtaa

Protein coding sequence Strain 26695 FutA (SEQ ID NO:12)

mfqplldafiesasiekmaskspppplkiavanwwgdeeikefkksvlyfilsqryaitlhqnpnefsdlvfsnplgaarkil
syqntkrvfytgenespnfnlfdyaigfdeldfndrylrmplyyahlhykaelvndttapyklkdnslyalkkpshhfkenh
pnlcavvndesdllkrgfasfvasnanapmrnafydalnsiepvtgggsvrntlgykvgnkseflsqykfnlcfensqgygy
vtekildayfshtipiywgspsvakdfnpksfvnvhdfnnfdeaidyikylhthpnayldmlyenplntldgkayfyqdlsf
kkildffktilendtiyhkfstsfmweydlhkplvsiddlrvnyddlrvnydrllqnaspllelsqnttfkiyrkayqkslpllrav
rklvkklgl*

FIGURE 7

<u>19C2A fucosyltransferase nucleotide sequence (SEQ ID NO:13)</u>

atgttccaacccttactagacgcctttatagaaagtgctccaatt

<u>19C2A predicted protein sequence (SEQ ID NO:14)</u>

mfqplldafiesapi

FIGURE 8

Protein sequence from strain 1182 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

```
Query:   23   PPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI   81
Sbjct:   11   TVPLLLAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSDCP   67

Query:   82   LSYQNAKRVFYTGEN---ESPNFNLF---DYAIGFDELDFRDRYLRMPLYYDRLHHKAES   135
Sbjct:   68   LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPPGQPWVWASMESPSNS   127

Query:  136   -VNDTTSPYKLKPDSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGPASFVASNPN-AP   193
Sbjct:  128   GLNDLRDGYFNWTLSYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNTRS   187

Query:  194   KRNAFYDVLNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGYVTEKIID   253
Sbjct:  188   KRERFYKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWK   247

Query:  254   -AYFSHTIPIYWGSPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYL   305
Sbjct:  248   NALQAGTIPVVLGPRAVYEDFVPPKSFIHVDDFKSPKELADYLLYLDTNPTAYS   301
```

FIGURE 9

Fucosyltransferase from strain 1111 FutA aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

```
Query:    27   IAVANWWGDEEIKKFKKSVLYFILSQHYTITLHRNPDKPADIVFG-NPLGSARKILSYQN   85
Sbjct:    16   LAIYTWWSLIEYKEWKKSPIYPIGSQAPQPPLR---ILLWTWPFNGNPLALSDCPLSYQN   72

Query:    86   AKRVFYTGEN---EVPNPNLF---DYAIGFDELDFRDRYLRMPLYYAYLHYKAEL-VNDT   138
Sbjct:    73   TARCRLTANRSPLESADAVLFHHRDLSKGPPDLPPSPRPPGQPWVWASMESPSNSGLNDL   132

Query:   139   TSPYKLQPDSLYALKKPSHHPKENHPNLCAVVNNESDPLKRGFASFVASNPN-APRRNAF   197
Sbjct:   133   RDGYFNWTLSYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNTRSKRERF   192

Query:   198   YEALNAIEPVAGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENTQGYGYVTEKIID-AYFS   256
Sbjct:   193   YKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWKNALQA   252

Query:   257   HTIPIYWGSPSVAKDFNP-KSFVNVHDFNNFDEAIDYIRYLHTHPNAYLDMHYENPLNTI   315
Sbjct:   253   GTIPVVLGPRAVYEDFVPPKSFIHVDDFKSPKELADYLLYLDTNPTAYS----------   301

Query:   316   DGKAYFYQNLSFKKILDFFKTILENDTIYHDNPFIFYRDLNEPSVSIDGLRVNYDDLRVN   375
Sbjct:   302   ----------------------------EYFEWRYDLRVRLFSWDALR---------   321

Query:   376   YDDLRVNYDDLRVNYERLLQNASPLLELSQNTTFKIYRKAYQ   417
Sbjct:   322   -------YDEGPCRVCRLLQNAPD-----RYKTYPNIAKWFQ   351
```

FIGURE 10

Protein sequence from strain 1218 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

```
Query:   23  PPPLKIAVANWWGDEEVEEFKKNILYFILSQHYTITLHQNPNEPSDLVFGS-PIGSARKI   81
Sbjct:   11  TVPLLLAIYTWWSLIEYKEWKKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSDCP. 67

Query:   82  LSYQNAKRVFYTGEN---ESPNFNLF---DYAIGFDELDFRDRYLRMPLYYDRLHHKAES  135
Sbjct:   68  LSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPPGQPWVWASMESPSNS  127

Query:  136  -VNDTTSPYKLKPDSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPN-AP  193
Sbjct:  128  GLNDLRDGYFNWTLSYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNTRS  187

Query:  194  KRNAFYDALNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGYVTEKIID  253
Sbjct:  188  KRERFYKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKLWK  247

Query:  254  -AYFSHTIPIYWGSPSVAQDFNP-KSFVNVCDFKDFDEAIDHVRYLHTHPNAYLDMLYEN  311
Sbjct:  248  NALQAGTIPVVLGPRAVYEDFVPPKSFIHVDDFKSPKELADYLLYLDTNPTAYS------  301

Query:  312  PLNTLDGKAYFYQNLSFKKILDFPKTILENDTIYHDNPFIPYRDLNEPLISIDDLRVNYD  371
Sbjct:  302  ------------------------------EYFEWRYDLRVRLFSWDALR--YD        323

Query:  372  DLRVNYDDLRVNYDDLRVNYDDLRVNYD  399
Sbjct:  324  EGFCRVCRLLQNAPDRYKTYPNIAKWFQ  351
```

FIGURE 11

Protein sequence from strain 19C2 FutB aligned with pfam00852, Glyco_transf_10, Glycosyltransferase family 10

```
Query:   22   PPLNIALANWWPLDKRESKGFRKKFILHFILSQHYTIALHRNPDKPADIVFG-NPLGSAR   80
Sbjct:   12   VPLLLAIYTWWSL--IEYKEW-KKSPIYFIGSQAPQPPLR---ILLWTWPFNGNPLALSD. 65

Query:   81   KILSYQNAKRVFYTGEN---EVPNFNLF---DYAIGFDELDFRDRYLRMPLYYDRLHHKA   134
Sbjct:   66   CPLSYQNTARCRLTANRSPLESADAVLFHHRDLSKGFPDLPPSPRPPGQPWVWASMESPS   125

Query:  135   ES-VNDTTAPYKIKSDSLYALKKPSHHFKENHPHLCALINNEIDPLKRGFASFVASNPN-   192
Sbjct:  126   NSGLNDLRDGYFNWTLSYRADSDAFHPYGYLEPRLSQVVNAPLLSAKRKGAAWVVSNCNT   185

Query:  193   APIRNAFYEALNSIEPVTGGGSVRNTLGYNVKNKNEFLSQYKFNLCFENTQGYGYVTEKI   252
Sbjct:  186   RSKRERFYKQLNKHLQVDVGGRVANPLPLKVGCLVETLSQYKFYLAFENSQHYDYVTEKL   245

Query:  253   ID-AYFSHTIPIYWGGVPSVAKDFNP   277
Sbjct:  246   WKNALQAGTIPVVLGP-RAVYEDFVP   270
```

FIGURE 12

```
                      1                                                50
1111FutA.pep     (1)  MFQPLLDAFIESAPIKKWPLN--LPPLKIAVANWWGDEEIKK---FKKSV
19C2A.pep        (1)  MFQPLLDAFIESAPI-----------------------------------
915A.pepneose    (1)  ----------------MASK-SPPLKIAVANWWGDEEIKK---FKKSV
26695A.pep       (1)  MFQPLLDAFIESASIEKMASKSPPPPLKIAVANWWGDEEIKE---FKKSV
1182B.pep        (1)  MFQPLLDAYIESASIEKITSKS-PPLKIAVANWWGDEEVEE---FKKNI
1218B.pep        (1)  MFQPLLDAYIESASIEKITSKS-PPLKIAVANWWGDEEVEE---FKKNI
ORF19C2B.pep     (1)  MFQPLLDAYIDSTRLDETDYK---PPLNIALANWWPLDKRESKGFRKKFI
Consensus        (1)  MFQPLLDAFIESA IEK  SK   PPLKIAVANWWGDEEI    FKK I


                      51                                               100
1111FutA.pep    (46)  LYFILSQHYTITLHRNPDKPADIVFGNPLGSARKILSYQNAKRVFYTGEN
19C2A.pep       (16)  -------------------------------------------------
915A.pepneose   (29)  LYFILSQHYTITLHRNPDKPADIVFGNPLGSARKILSYQNAKRVFYTGEN
26695A.pep      (48)  LYFILSQRYAITLHQNPNEFSDLVFSNPLGAARKILSYQNTKRVFYTGEN
1182B.pep       (47)  LYFILSQHYTITLHQNPNEPSDIVFGSPIGSARKILSYQNAKRVFYTGEN
1218B.pep       (47)  LYFILSQHYTITLHQNPNEPSDIVFGSPIGSARKILSYQNAKRVFYTGEN
ORF19C2B.pep    (48)  LHFILSQHYTIALHRNPDKPADIVFGNPLGSARKILSYQNAKRVFYTGEN
Consensus       (51)  LYFILSQHYTITLH NP  PADIVFGNPLGSARKILSYQNAKRVFYTGEN


                      101                                              150
1111FutA.pep    (96)  EVPNFNLFDYAIGFDELDFRDRYLRMPLYYAYIHYKAELVNDTTSPYKLQ
19C2A.pep       (16)  -------------------------------------------------
915A.pepneose   (79)  EVPNFNLFDYAIGF-----------------------------------
26695A.pep      (98)  ESPNFNLFDYAIGFDELDFNDRYLRMPLYYAHLHYKAELVNDTTAPYKLK
1182B.pep       (97)  ESPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHKAESVNDTTSPYKLK
1218B.pep       (97)  ESPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHKAESVNDTTSPYKLK
ORF19C2B.pep    (98)  EVPNFNLFDYAIGFDELDFRDRYLRMPLYYDRLHHKAESVNDTTAPYKLK
Consensus      (101)  E PNFNLFDYAIGFDELDFRDRYLRMPLYY  LHHKAE VNDTTSPYKLK


                      151                                              200
1111FutA.pep   (146)  PDSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPNAPRRN
19C2A.pep       (16)  -------------------------------------------------
915A.pepneose   (93)  -------------------------------------------------
26695A.pep     (148)  DNSLYALKKPSHHFKENHPNLCAVVNDESDLLKRGFASFVASNANAPMRN
1182B.pep      (147)  PDSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPNAHKRN
1218B.pep      (147)  PDSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPNAHKRN
ORF19C2B.pep   (148)  SDSLYALKKPSHHFKENHPHLCALINNEIDPLKRGFASFVASNPNAHIRN
Consensus      (151)  DSLYALKKPSHHFKENHPNLCAVVNNESDPLKRGFASFVASNPNAP RN


                      201                                              250
1111FutA.pep   (196)  AFYEALNAIEPVAGGGSVKNTLGYNVKNKSEFLSQYKFNLCFENTQGYGY
19C2A.pep       (16)  -------------------------------------------------
915A.pepneose   (93)  -------------------------------------------------
26695A.pep     (198)  AFYDALNSIEPVTGGGSVRNTLGYKVGNKSEFLSQYKFNLCFENSQGYGY
1182B.pep      (197)  AFYDVLNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGY
1218B.pep      (197)  AFYDALNSIEPVIGGGSVKNTLGYNIKNKSEFLSQYKFNLCFENSQGYGY
ORF19C2B.pep   (198)  AFYEALNSIEPVTGGGSVRNTLGYNVKNKNEFLSQYKFNLCFENTQGYGY
Consensus      (201)  AFYDALNSIEPV GGGSVKNTLGYNVKNKSEFLSQYKFNLCFENSQGYGY
```

FIGURE 13

```
                           1                                                50
      1111FutA      (1)  ATGTTCCAACCCCTATTAGATGCCTTTATAGAAAGCGCT-CCATTGAAAA
915A.cod(MWG)       (1)  ATGTTCCAACCCCTATTAGATGCCTTTATAGAAAGCGCTTCCATTGAAAA
  19C2FutA.cod      (1)  ATGTTCCAACCCTTACTAGACGCCTTTATAGAAAGTGCTCCAATT-----
    26695A.cod      (1)  ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA
         1182B      (1)  ATGTTCCAACCCCTATTAGACGCTTATATAGAAAGCGCTTCCATTGAAAA
     1218B.nuc      (1)  ATGTTCCAACCCCTATTAGACGCTTATATAGAAAGCGCTTCCATTGAAAA
      ORF19C2B      (1)  ATGTTCCAACCCCTATTAGACGCTTATATAGACAGCACCCGTTTAGATGA
     Consensus      (1)  ATGTTCCAACCCCTATTAGACGCCTTTATAGAAAGCGCTTCCATTGAAAA

                           51                                               100
      1111FutA     (50)  AATGGCCTCTAAATCTCGCCCCCC-----TAAAAATCGCTGTGGCGAATT
915A.cod(MWG)      (51)  AATGGCCTCTAAATCTCCCCCCC------TAAAAATCGCTGTGGCGAATT
  19C2FutA.cod     (46)  --------------------------------------------------
    26695A.cod     (51)  AATGGCCTCTAAATCTCGCCCCCCCCCCCTAAAAATCGCTGTGGCGAATT
         1182B     (51)  AATTACCTCTAAATCTCCCCCCCCCC---TAAAAATCGCTGTGGCGAATT
     1218B.nuc     (51)  AATTACCTCTAAATCTCCCCCCCCCC---TAAAAATCGCTGTGGCGAATT
      ORF19C2B     (51)  AACCGATTATAA------GCCCCCAT---TAAATATAGCCCTAGCGAATT
     Consensus     (51)  AAT GCCTCTAAATCTCCCCCCCC        TAAAAATCGCTGTGGCGAATT

                           101                                              150
      1111FutA     (95)  GGTGG-----GGAGATGA-AGAAATTAAAAAAATTTAAAAAGAGCGTTCTT
915A.cod(MWG)      (95)  GGTGG-----GGAGATGA-AGAAATTAAAAAAATTTAAAAAGAGCGTTCTT
  19C2FutA.cod     (46)  --------------------------------------------------
    26695A.cod    (101)  GGTGG-----GGAGATGA-AGAAATTAAAGAATTTAAAAAGAGCGTTCTT
         1182B     (98)  GGTGG-----GGAGATGA-AGAGGTTGAAGAATTTAAAAAGAACATTCTT
     1218B.nuc     (98)  GGTGG-----GGAGATGA-AGAGGTTGAAGAATTTAAAAAGAACATTCTT
      ORF19C2B     (92)  GGTGGCCTTTGGATAAAAGAGAAAGCAAAGGGTTTAGAAAAAAATTTATC
     Consensus    (101)  GGTGG     GGAGATGA AGAAATTAAAGAATTTAAAAAGA C TTCTT

                           151                                              200
      1111FutA    (139)  T---ATTTTATCCTAAGCCAGCATTACACAATCAGTTTACACCGAAACCC
915A.cod(MWG)     (139)  T---ATTTTATCCTAAGCCAGCATTACACAATCAGTTTACACCGAAACCC
  19C2FutA.cod     (46)  --------------------------------------------------
    26695A.cod    (145)  T---ATTTTATCCTAAGCCAACGCTACGCAATCACCCTCGACCAAAACCG
         1182B    (142)  T---ATTTTATTCTCAGTCAGCATTACACAATCACCGTCGACCAAAACCG
     1218B.nuc    (142)  T---ATTTTATTCTCAGTCAGCATTACACAATCACCCTCCACCAAAACCC
      ORF19C2B    (142)  TTACATTTCATTTTAAGTCAGCATTACACAATCGGTCTCCACCGAAACCC
     Consensus    (151)  T   ATTTTAT CTAAG CAGCATTACACAATCAC CTCCACC AAACCC

                           201                                              250
      1111FutA    (186)  TGATAAACCTGCGGACATCGTCTTTGGTAACCCCCTTGGATCAGCCAGAA
915A.cod(MWG)     (186)  TGATAAACCTGCGGACATCGTCTTTGGTAACCCCCTTGGATCAGCCAGAA
  19C2FutA.cod     (46)  --------------------------------------------------
    26695A.cod    (192)  CAATGAATTTTCAGATCTAGTTTTTAGCAATCCTCTTGGAGCGGCTAGAA
         1182B    (189)  CAACGAACCCTCCGATCTCGTCTTTGGCAGTCCTATTGGATCAGCCAGAA
     1218B.nuc    (189)  CAACGAACCCTCCGATCTCGTCTTTGGCAGTCCTATTGGATCAGCCAGAA
      ORF19C2B    (192)  TGATAAACCTGCGGACATCGTTTTTGGTAACCCCCTTGGATCAGCCAGAA
     Consensus    (201)  AT AACCT C GA TCGTCTTTGG AA CC CTTGGATCAGCCAGAA
```

FIG. 13 (CONT)

```
                         251                                                 300
    1111FutA    (236)  AAATCTTATCCTATCAAAACGCAAAAAGGGTGTTTTACACCGGTGAAAAT
915A.cod(MWG)   (236)  AAATCTTATCCTATCAAAACGCAAAAAGGGTGTTTTACACCGGTGAAAAT
 19C2FutA.cod    (46)  --------------------------------------------------
   26695A.cod   (242)  AGATTTTATCTTATCAAAACACTAAACGAGTGTTTTACACCGGTGAAAAC
        1182B   (239)  AAATCTTATCCTATCAAAACGCAAAAAGAGTGTTTTACACCGGTGAAAAC
     1218B.nuc  (239)  AAATCTTATCCTATCAAAACGCAAAAAGAGTGTTTTACACCGGTGAAAAC
      ORF19C2B  (242)  AAATCCTATCCTATCAAAACGGTAAAAGGGTGTTTTACACCGGTGAAAAC
     Consensus  (251)  AAATCTTATCCTATCAAAACGCAAAAAG GTGTTTTACACCGGTGAAAAC

                         301                                                 350
    1111FutA    (286)  GAAGTCCCTAACTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
915A.cod(MWG)   (286)  GAAGTCCCTAACTTCAACCTCTTTGATTACGCCATAGGCTTTTGATGA--
 19C2FutA.cod    (46)  --------------------------------------------------
   26695A.cod   (292)  GAATCACCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
        1182B   (289)  GAATCGCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
     1218B.nuc  (289)  GAATCGCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
      ORF19C2B  (292)  GAAGTCCCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT-GATGAAT
     Consensus  (301)  GAA   CCTAATTTCAACCTCTTTGATTACGCCATAGGCTTT GATGAAT

                         351                                                 400
    1111FutA    (335)  TGGACTTTAGAGATCGTTATTTGAGAATGCCTTTGTATTATGCCTATTTG
915A.cod(MWG)   (334)  --------------------------------------------------
 19C2FutA.cod    (46)  --------------------------------------------------
   26695A.cod   (341)  TGGATTTTAATGATCGTTATTTGAGAATGCCTTTGTATTATGCCCATTTG
        1182B   (338)  TGGATTTTAGAGATCGTTATTTAAGAATGCCTTTATATTATGATAGACTA
     1218B.nuc  (338)  TGGATTTTAGAGATCGTTATTTAAGAATGCCTTTATATTATGATAGACTA
      ORF19C2B  (341)  TGGACTTTAGAGATCGTTATTTGAGAATGCCTTTATATTATGATAGACTA
     Consensus  (351)  TGGA TTTAGAGATCGTTATTT AGAATGCCTTT TATTATG        T

                         401                                                 450
    1111FutA    (385)  CATTATAAAGCCGAGCTTGTTAATGACACCACTTCGCCTTATAAACTCCA
915A.cod(MWG)   (334)  --------------------------------------------------
 19C2FutA.cod    (46)  --------------------------------------------------
   26695A.cod   (391)  CAGTATAAAGCCGAGCTTGTTAATGACACCACTGCGCCCTACAAACTCAA
        1182B   (388)  CACCATAAAGCCGAGAGCGTGAATGACACCACTTCGCCTTACAAACTCAA
     1218B.nuc  (388)  CACCATAAAGCCGAGAGCGTGAATGACACCACTTCGCGTTACAAACTCAA
      ORF19C2B  (391)  CACCATAAAGCCGAGAGCGTGAATGACACCACCGCACCTTACAAGATTAA
     Consensus  (401)  CAC ATAAAGCCGAG   GT AATGACACCACT CGCCTTACAAACTCAA

                         451                                                 500
    1111FutA    (435)  ACCTGACAGCCTTTATGCTTTAAAAAAACCCTCCATCATTTTAAAGAAA
915A.cod(MWG)   (334)  -------------------------------------------------
 19C2FutA.cod    (46)  -------------------------------------------------
   26695A.cod   (441)  AGACAACAGCCTTTATGCTTTAAAAAAAACCCTCTCATCATTTTAAAGAAA
        1182B   (438)  ACCTGACAGCCTTTATGCTTTAAAAAAAACCCTCCATCATTTTAAAGAAA
     1218B.nuc  (438)  ACCTGACAGCCTTTATGCTTTAAAAAAAACCCTCGCATCATTTTAAAGAAA
      ORF19C2B  (441)  ATCTGACAGCCTTTATGCTTTAAAAAAGCCCTCCATCATTTTAAAGAAA
     Consensus  (451)  A CTGACAGCCTTTATGCTTTAAAAAAACCCTCCATCATTTTAAAGAAA
```

FIG.13 (CONT)

```
                          501                                               550
     1111FutA    (485) ACCACCCCAATTTGTGCGCAGTAGTGAATAATGAGAGTGATCCTTTGAAA
 915A.cod(MWG)   (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
    26695A.cod   (491) ACCACCCTAATTTGTGCGCAGTAGTGAATGATGAGAGCGATCTTTTAAAA
         1182B   (488) ACCACCCCAATTTATGCGCAGTAGTGAACAATGAGAGCGATCCTTTGAAA
     1218B.nuc   (488) ACCACCCCAATTTATGCGCAGTAGTGAACAATGAGAGCGATCCTTTGAAA
      ORF19C2B   (491) ACCACCCACATTTATGCGCGCTAATCAATAATGAGATCGATCCTTTGAAA
     Consensus   (501) ACCACCC AATTT TGCGCAGTAGTGAA AATGAGAGCGATCCTTTGAAA

                          551                                               600
     1111FutA    (535) AGAGGGTTTGCGAGCTTTGTCGCAAGCAACCCTAACGCTCCTAGAAGGAA
 915A.cod(MWG)   (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
    26695A.cod   (541) AGAGGGTTTGCCAGTTTTGTAGCGAGCAACGCTAACGCTCCTATGAGGAA
         1182B   (538) AGAGGGTTTGCGAGTTTTGTAGCGAGCAACCCTAACGCTCCTAAAAGGAA
     1218B.nuc   (538) AGAGGGTTTGCGAGTTTTGTAGCGAGCAACCCTAACGCTCCTAAAAGGAA
      ORF19C2B   (541) AGAGGGTTTGCGAGCTTTGTCGCAAGCAACCCTAACGCCCCTATAAGGAA
     Consensus   (551) AGAGGGTTTGCGAG TTTGT GC AGCAACCCTAACGCTCCTA AAGGAA

                          601                                               650
     1111FutA    (585) CGCTTTTTATGAGGCTTTAAACGCTATTGAGCCAGTTGCTGGGGGAGGGA
 915A.cod(MWG)   (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
    26695A.cod   (591) CGCTTTTTATGACGCTCTAAATTCCATAGAGCCAGTTACTGGGGGAGGAA
         1182B   (588) TGCTTTCTATGACGTTTTAAATTCTATAGAGCCAGTTATTGGGGGAGGGA
     1218B.nuc   (588) TGCTTTCTATGACGCTTTAAATTCTATAGAGCCAGTTATTGGGGGAGGGA
      ORF19C2B   (591) CGCTTTCTATGAGGCTTTAAATTCTATTGAGCCAGTTACTGGGGGAGGGA
     Consensus   (601)  GCTTT TATGA GCTTTAAATTCTAT GAGCCAGTTA TGGGGGAGGGA

                          651                                               700
     1111FutA    (635) GCGTGAAAAACACTTTAGGCTATAATGTCAAAAACAAGAGCGAGTTTTTA
 915A.cod(MWG)   (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
    26695A.cod   (641) GTGTGAGAAACACTTTAGGCTATAAGGTTGGAAACAAAAGCGAGTTTTTA
         1182B   (638) GCGTGAAAAACACTTTAGGCTATAACATTAAAAAACAAGAGCGAGTTTTTA
     1218B.nuc   (638) GCGTGAAAAACACTTTAGGCTATAACATTAAAAAACAAGAGCGAGTTTTTA
      ORF19C2B   (641) GCGTGAGAAACACTTTAGGCTATAACGTCAAAAACAAAAACGAATTTTTG
     Consensus   (651) GCGTGA AAACACTTTAGGCTATAA  T AAAAACAA AGCGAGTTTTTA

                          701                                               750
     1111FutA    (685) AGCCAATACAAATTCAATCTGTGTTTTGAAAACACTCAAGGCTATGGCTA
 915A.cod(MWG)   (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
    26695A.cod   (691) AGCCAATACAAGTTCAATCTCTGTTTTGAAAACTCGCAAGGTTATGGCTA
         1182B   (688) AGCCAATACAAATTCAATCTGTGTTTTGAAAACTCACAAGGCTATGGCTA
     1218B.nuc   (688) AGCCAATACAAATTCAATCTGTGTTTTGAAAACTCACAAGGCTATGGCTA
      ORF19C2B   (691) AGCCAATACAAGTTCAATCTGTGCTTTGAAAACAGTCAAGGCTATGGCTA
     Consensus   (701) AGCCAATACAA TTCAATCTGTGTTTTGAAAAC C CAAGGCTATGGCTA
```

FIG. 13 (CONT.)

```
                    751                                            800
1111FutA      (735) TGTAACTGAAAAGATCATTGACGGCTTATTTCAGCCATACCATTCCTATTT
915A.cod(MWG) (334) --------------------------------------------------
19C2FutA.cod   (46) --------------------------------------------------
26695A.cod    (741) TGTAACCGAAAAAATCCTTGATGCGTATTTTAGCCATACCATTCCTATTT
1182B         (738) TGTAACTGAAAAAATCATTGACGGCTTACTTTAGCCATACCATTCCTATTT
1218B.nuc     (738) TGTAACTGAAAAAATCATTGACGGCTTACTTTAGCCATACCATTCCTATTT
ORF19C2B      (741) TGTTACTGAAAAAATCATTGACGGCTTACTTCAGCCACACCATTCCTATTT
Consensus     (751) TGTAACTGAAAAAATCATTGACGCTTA TT AGCCATACCATTCCTATTT


                    801                                            850
1111FutA      (785) ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTTAACCCTAAGAGTTTT
915A.cod(MWG) (334) --------------------------------------------------
19C2FutA.cod   (46) --------------------------------------------------
26695A.cod    (791) ATTGGGGG--AGTCC-CAGCGTGGCGAAAGATTTTAACCCTAAAAGTTTT
1182B         (788) ATTGGGGG--AGTCC-TAGCGTGGCACAAGATTTTAACCCTAAGAGTTTT
1218B.nuc     (788) ATTGGGGG--AGTCC-TAGCGTGGCACAAGATTTTAACCCTAAGAGTTTT
ORF19C2B      (791) ATTGGGGGGGAGTCCCTAGCGTGGCGAAAGATTTTAACCCC--------
Consensus     (801) ATTGGGGG AGTCC AGCGTGGC AAGATTTTAACCCTAA AGTTTT


                    851                                            900
1111FutA      (832) GTGAATGTCCATGATTTCAACAACTTTGATGAAGCGATTGACTATATCAG
915A.cod(MWG) (334) --------------------------------------------------
19C2FutA.cod   (46) --------------------------------------------------
26695A.cod    (838) GTGAATGTGCATGATTTCAACAACTTTGATGAAGCGATTGATTATATCAA
1182B         (835) GTGAATGTTTGTGATTTTAAAGATTTTGATGAAGCGATTGATCATGTGCG
1218B.nuc     (835) GTGAATGTTTGTGATTTTAAAGATTTTGATGAAGCGATTGATCATGTGCG
ORF19C2B      (832) --------------------------------------------------
Consensus     (851) GTGAATGT   TGATTT AA  A TTTGATGAAGCGATTGA  AT T


                    901                                            950
1111FutA      (882) ATACTTGCACACGCACCCAAACGGCTTATTTAGACATGGACTATGAAAACG
915A.cod(MWG) (334) --------------------------------------------------
19C2FutA.cod   (46) --------------------------------------------------
26695A.cod    (888) ATACCTGCACACGCACCGAAACGCTTATTTAGACATGCTCTATGAAAACG
1182B         (885) ATACTTGCACACGCACCCAAACGCTTATTTAGACATGCTTTATGAAAACG
1218B.nuc     (885) ATACTTGCACACGCACCCAAACGCTTATTTAGACATGCTTTATGAAAACG
ORF19C2B      (832) --------------------------------------------------
Consensus     (901) ATAC TGCACACGCACCCAAACGCTTATTTAGACATGC  TATGAAAACC


                    951                                           1000
1111FutA      (932) CTTTAAACACTATTGATGGGAAAGCTTACTTTTACCAAAATTTGAGTTTT
915A.cod(MWG) (334) --------------------------------------------------
19C2FutA.cod   (46) --------------------------------------------------
26695A.cod    (938) CTTTAAACACCCTTGATGGGAAAGCTTACTTTTACCAAGATTTGAGTTTT
1182B         (935) CTTTAAACACCCTTGATGGGAAAGCTTACTTTTACCAAAATTTGAGTTTT
1218B.nuc     (935) CTTTAAACACCCTTGATGGGAAAGCTTACTTTTACCAAAATTTGAGTTTT
ORF19C2B      (832) --------------------------------------------------
Consensus     (951) CTTTAAACAC  TTGATGGGAAAGCTTACTTTTACCAA ATTTGAGTTTT
```

FIG. 13 (CONT)

```
                       1001                                          1050
     1111FutA    (982) AAAAAAATCCTAGATTTTTTTAAAACGATTTTAGAAAACGACACGATCTA
915A.cod(MWG)    (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
   26695A.cod    (988) AAAAAAATCCTAGATTTTTTTAAAACGATTTTTAGAAAACGATACGATTTA
        1182B    (985) AAAAAAATCCTAGATTTTTTTAAAACGATTTTAGAAAACGACACGATTTA
    1218B.nuc    (985) AAAAAAATCCTAGATTTTTTTAAAACGATCTTAGAAAACGACACGATTTA
     ORF19C2B    (832) --------------------------------------------------
    Consensus   (1001) AAAAAAATCCTAGATTTTTTTAAAACGAT TTAGAAAACGA ACGAT TA

                       1051                                          1100
     1111FutA   (1032) TCACGATAACCC------TTTCATTTTCTATCGTGATTGAATGAGCCTT
915A.cod(MWG)    (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
   26695A.cod   (1038) TCACAAATTCTCAACATCTTTCATGTGGGAGTACGATCTGCATAAGCCGT
        1182B   (1035) TCACGATAACCC------TTTTATTTTTTATCGTGATTGAATGAGCCGT
    1218B.nuc   (1035) TCACGATAACCC------TTTTATTTTTTATCGTGATTTGAATGAGCCGT
     ORF19C2B    (832) --------------------------------------------------
    Consensus   (1051) TCAC A   C C       TTT AT T  A     GAT TG AT AGCC T

                       1101                                          1150
     1111FutA   (1076) CAGTATCTATTGATGGT---TTGAGGGTTAATTATGATGATTTGAGGGTT
915A.cod(MWG)    (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
   26695A.cod   (1088) TAGTATCCATTGATGAT---TTGAGGGTTAATTATGATGATTTGAGGGTT
        1182B   (1079) TAATATCTATTGATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTT
    1218B.nuc   (1079) TAATATCTATTGATGAT---TTGAGGGTTAATTATGATGATTTGAGGGTT
     ORF19C2B    (832) --------------------------------------------------
    Consensus   (1101)  A TATC ATTGATG T   TTGAGGGTTAATTATGATGATTTGAGGGTT

                       1151                                          1200
     1111FutA   (1123) AATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGA
915A.cod(MWG)    (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
   26695A.cod   (1135) AATTATGACCGGCTTTTACAAAACGCTTCGCCTTTATTAGAACTCTCTCA
        1182B   (1129) AATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGA
    1218B.nuc   (1126) AATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGA
     ORF19C2B    (832) --------------------------------------------------
    Consensus   (1151) AATTATGA      T      AA   T      TTT   G     T T A

                       1201                                          1250
     1111FutA   (1173) GCGCCTTTTACAAAACGCCTCGCCTTTATTAGAACTCTCTCAAAACACCA
915A.cod(MWG)    (334) --------------------------------------------------
 19C2FutA.cod     (46) --------------------------------------------------
   26695A.cod   (1185) AAACACCACTTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCTT
        1182B   (1179) TGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGA
    1218B.nuc   (1176) TGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGA
     ORF19C2B    (832) --------------------------------------------------
    Consensus   (1201)                   AA
```

FIG. 13 (CONT)

```
                    1251                                              1300
     1111FutA  (1223) CTTTTAAAATCTATCGCAAAGCTTATCAAAAATCCTTGCCTTTGTTGCGT
 915A.cod(MWG)  (334) --------------------------------------------------
  19C2FutA.cod   (46) --------------------------------------------------
    26695A.cod (1235) TGTTGCGCGCGGTGAGAAAGTTGGTTAAAAAATTGGGTTTGTAA------
         1182B (1229) GGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAAT
     1218B.nuc (1226) GGGTTAATTATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAAT
      ORF19C2B  (832) --------------------------------------------------
     Consensus (1251)    T                        T A  A
```

```
                    1301                                              1350
     1111FutA  (1273) GCCATAAGGAGATGGGTTAAAAAGTAA-----------------------
 915A.cod(MWG)  (334) --------------------------------------------------
  19C2FutA.cod   (46) --------------------------------------------------
    26695A.cod (1279) --------------------------------------------------
         1182B (1279) TATGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGAGCG
     1218B.nuc (1276) TGTGATGATTTGAGGGTTAATTATGATGATTTGAGGGTTAATTATGAGCG
      ORF19C2B  (832) --------------------------------------------------
     Consensus (1301)
```

```
                    1351                                              1400
     1111FutA  (1300) --------------------------------------------------
 915A.cod(MWG)  (334) --------------------------------------------------
  19C2FutA.cod   (46) --------------------------------------------------
    26695A.cod (1279) --------------------------------------------------
         1182B (1329) GCTCTTACAAAACGCCTCGCCTTTATTAGAACTCTCTCAAAACACCACTT
     1218B.nuc (1326) GCTCTTACAAAACGCCTCGCCTTTATTAGAACTCTCTCAAAACACCACTT
      ORF19C2B  (832) --------------------------------------------------
     Consensus (1351)
```

```
                    1401                                              1450
     1111FutA  (1300) --------------------------------------------------
 915A.cod(MWG)  (334) --------------------------------------------------
  19C2FutA.cod   (46) --------------------------------------------------
    26695A.cod (1279) --------------------------------------------------
         1182B (1379) TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTTGTTGCGTGCG
     1218B.nuc (1376) TTAAAATCTATCGCAAAGCTTATCAAAAATCCTTACCTTTGTTGCGTGCG
      ORF19C2B  (832) --------------------------------------------------
     Consensus (1401)
```

```
                    1451                     1483
     1111FutA  (1300) --------------------------------
 915A.cod(MWG)  (334) --------------------------------
  19C2FutA.cod   (46) --------------------------------
    26695A.cod (1279) --------------------------------
         1182B (1429) GCGAGAAAGTTGATTAAAAAATTGGGTTTGTAA
     1218B.nuc (1426) GCGAGAAAGTTGATTAAAAAATTGGGTTTGTAA
      ORF19C2B  (832) --------------------------------
     Consensus (1451)
```

FIG. 14

Oligo Structures

Lacto-<u>N</u>-neo-Tetraose (LNnT)

Galβ1-4GlcNAcβ1-3Galβ1-4Glc

Lacto-<u>N</u>-Fucopentaose III (LNFP III)

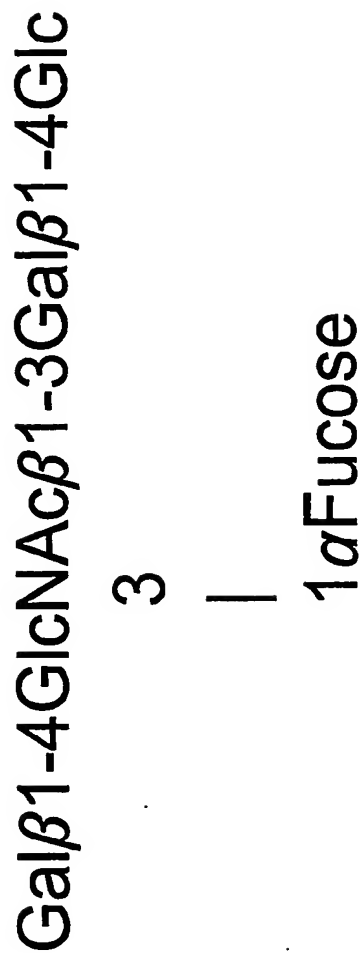Galβ1-4GlcNAcβ1-3Galβ1-4Glc

3
|
1αFucose

Linkage Analysis by GC/MS

The samples were methylated, hydrolyzed, reduced with sodium borodeuteride, acetylated and analyzed by GC/MS along with samples of LNnT and LNF3.

♠ A Glc vs. Glc-NAc value close to 1 favors fucosylation of Glc-NAc.

♠ A Glc vs. Glc-NAc value close to 0 favors fucosylation of Glc

FIG.15

H. Pylori Strain	Glc vs. Glc-NAc
915A2	0.982
19C2A5	0.040
1111A2	0.975
19C2B1	0.991
1182B3	0.983

FIG. 16

1 Liter LNFIII Synthesis

Batch Number	Resin Type	Total Yield	Actual Percent Recovery
1-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.567 g	61%
2-02	MR3 NH_4HCO_3 column (1ml resin/1ml synthesis)	1.760 g	68%
3-02	Dowex1/Dowex 50 (2ml resin/1ml synthesis)	1.221 g	47%

FIG. 17